

## RAW SEQUENCE LISTING

DATE: 09/24/2003

PATENT APPLICATION: US/10/663,451

TIME: 15:32:21

Input Set : N:\CrF3\RULE60\US10663451.raw.txt

Output Set: N:\CRF4\09242003\J663451.raw

49	Ser	Lys	Lys	Lys	Lys	Asn	Val	Thr	Met	Arg	Ser	Ile	Lys	Thr	Thr	Arg	
50				40					45					50			
51	gac	cga	gtg	cct	aca	tat	cag	tac	aac	atg	aat	ttt	gaa	aag	ctg	ggc	247
52	Asp	Arg	Val	Pro	Thr	Tyr	Gln	Tyr	Asn	Met	Asn	Phe	Glu	Lys	Leu	Gly	
53			55				60					65					
54	aaa	tgc	atc	ata	ata	aac	aac	aag	aac	ttt	gat	aaa	gtg	aca	ggt	atg	295
55	Lys	Cys	Ile	Ile	Ile	Asn	Asn	Lys	Asn	Phe	Asp	Lys	Val	Thr	Gly	Met	
56		70					75					80					
57	ggc	gtt	cga	aac	gga	aca	gac	aaa	gat	gcc	gag	gcg	ctc	ttc	aag	tgc	343
58	Gly	Val	Arg	Asn	Gly	Thr	Asp	Lys	Asp	Ala	Glu	Ala	Leu	Phe	Lys	Cys	
59		85				90					95					100	
60	ttc	cga	agc	ctg	ggt	ttt	gac	gtg	att	gtc	tat	aat	gac	tgc	tct	tgt	391
61	Phe	Arg	Ser	Leu	Gly	Phe	Asp	Val	Ile	Val	Tyr	Asn	Asp	Cys	Ser	Cys	
62				105						110				115			
63	gcc	aag	atg	caa	gat	ctg	ctt	aaa	aaa	gct	tct	gaa	gag	gac	cat	aca	439
64	Ala	Lys	Met	Gln	Asp	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Glu	Asp	His	Thr	
65				120						125				130			
66	aat	gcc	gcc	tgc	ttc	gcc	tgc	atc	ctc	tta	agc	cat	gga	gaa	gaa	aat	487
67	Asn	Ala	Ala	Cys	Phe	Ala	Cys	Ile	Leu	Leu	Ser	His	Gly	Glu	Glu	Asn	
68			135					140					145				
69	gta	att	tat	ggg	aaa	gat	ggt	gtc	aca	cca	ata	aag	gat	ttg	aca	gcc	535
70	Val	Ile	Tyr	Gly	Lys	Asp	Gly	Val	Thr	Pro	Ile	Lys	Asp	Leu	Thr	Ala	
71		150					155						160				
72	cac	ttt	agg	ggg	gat	aga	tgc	aaa	acc	ctt	tta	gag	aaa	ccc	aaa	ctc	583
73	His	Phe	Arg	Gly	Asp	Arg	Cys	Lys	Thr	Leu	Leu	Glu	Lys	Pro	Lys	Leu	
74		165				170					175					180	
75	ttc	ttc	att	cag	gct	tgc	cga	ggg	acc	gag	ctt	gat	gat	ggc	atc	cag	631
76	Phe	Phe	Ile	Gln	Ala	Cys	Arg	Gly	Thr	Glu	Leu	Asp	Asp	Gly	Ile	Gln	
77				185						190				195			
78	gcc	gac	tcg	ggg	ccc	atc	aat	gac	aca	gat	gct	aat	cct	cga	tac	aag	679
79	Ala	Asp	Ser	Gly	Pro	Ile	Asn	Asp	Thr	Asp	Ala	Asn	Pro	Arg	Tyr	Lys	
80				200						205				210			
81	atc	cca	gtg	gaa	gct	gac	ttc	ctc	ttc	gcc	tat	tcc	acg	gtt	cca	ggc	727
82	Ile	Pro	Val	Glu	Ala	Asp	Phe	Leu	Phe	Ala	Tyr	Ser	Thr	Val	Pro	Gly	
83			215					220					225				
84	tat	tac	tcg	tgg	agg	agc	cca	gga	aga	ggc	tcc	tgg	ttt	gtg	caa	gcc	775
85	Tyr	Tyr	Ser	Trp	Arg	Ser	Pro	Gly	Arg	Gly	Ser	Trp	Phe	Val	Gln	Ala	
86		230					235					240					
87	ctc	tgc	tcc	atc	ctg	gag	gag	cac	gga	aaa	gac	ctg	gaa	atc	atg	cag	823
88	Leu	Cys	Ser	Ile	Leu	Glu	Glu	His	Gly	Lys	Asp	Leu	Glu	Ile	Met	Gln	
89		245				250					255					260	
90	atc	ctc	acc	agg	gtg	aat	gac	aga	gtt	gcc	agg	cac	ttt	gag	tct	cag	871
91	Ile	Leu	Thr	Arg	Val	Asn	Asp	Arg	Val	Ala	Arg	His	Phe	Glu	Ser	Gln	
92				265						270				275			
93	tct	gat	gac	cca	cac	ttc	cat	gag	aag	aag	cag	atc	ccc	tgt	gtg	gtc	919
94	Ser	Asp	Asp	Pro	His	Phe	His	Glu	Lys	Lys	Gln	Ile	Pro	Cys	Val	Val	
95				280						285				290			
96	tcc	atg	ctc	acc	aag	gaa	ctc	tac	ttc	agt	caa	tag	ccat	atc	cagg		965
97	Ser	Met	Leu	Thr	Lys	Glu	Leu	Tyr	Phe	Ser	Gln						

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98          295          300
99      ggtacattct agctgagaag caatgggtca ctcattaatg aatcacattt ttttatgctc 1025
100      ttgaaatatt cagaaattct ccaggatttt aatttcagga aaatgtattg attcaacagg 1085
101      gaagaaactt tctggtgctg tcttttggtc tctgaatttt cagagacttt tttataatgt 1145
102      tattcatttg gtgactgtgt aactttctct taagattaat tttctctttg tatgtctggt 1205
103      accttgttaa tagacttaat acatgcaaca gaagtgaact ctggagaaaag ctcatggctg 1265
104      tgtccactgc aattgggtgt aacagtggta gagtcatggt tgcacttggc aaaaagaatc 1325
105      ccaatgtttg acaaaacaca gccaagggga tatttactgc tctttattgc agaattgtggg 1385
106      tattgagtgt gatttgaatg atttttcatt ggcttagggc agattttcat gcaaaagttc 1445
107      tcatatgagt tagaggagaa aaagcttaat gattctgata tgtatccatc aggatccagt 1505
108      ctggaaaaca gaaaccattc taggtgtttc aacagagggga gtttaataca ggaaattgac 1565
109      ttacatagat gataaaagag aagccaaaca gcaagaagct gttaccacac ccagggctat 1625
110      gaggataatg ggaagagggt tggtttcctg tgtccagtag tgggatcatc cagaggagct 1685
111      ggaaccatgg tgggggctgc ctagtgggag ttaggaccac caatggattg tggaaaatgg 1745
112      agccatgaca agaacaaagc cactgactga gatggagtga gctgagacag ataagagaat 1805
113      accttgctct acctatcctg ccctcacatc ttccaccagc accttactgc ccaggcctat 1865
114      ctggaagcca cctcaccaag gaccttgga gagcaaggga cagtgaggca ggagaagaac 1925
115      aagaaatgga tgtaagcctg gcccataatg tgaacataag taatcactaa tgctcaacaa 1985
116      tttatccatt caatcattta ttcattgggt tgtcagatag tctatgtatg tgtaaaacaa 2045
117      tctgttttgg ctttatgtgc aaaatctggt atagctttta aatatatctg gaacttttta 2105
118      gattattcca agccttattt tgagtaaata tttgttactt ttagttctat aagtgaggaa 2165
119      gagtttatgg caaagatttt tggcactttg ttttcaagat ggtgttatct tttgaattct 2225
120      tgataaatga ctgttttttt ctgcctaata gtaactgggt aaaaaacaaa tgttcatatt 2285
121      tattgattaa aaatgtggtt gctt
122      2309
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 26
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: PCR Primer
129 <400> SEQUENCE: 4
130      attggtggtgta acagtggtag agtcat
131      26
132 <210> SEQ ID NO: 5
133 <211> LENGTH: 20
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <223> OTHER INFORMATION: PCR Primer
138 <400> SEQUENCE: 5
139      cccttggtctg tgttttgtca
140      20
141 <210> SEQ ID NO: 6
142 <211> LENGTH: 27
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: PCR Probe
147 <400> SEQUENCE: 6
148      ttgcacttgg caaaaagaat cccaatg
149      27
150 <210> SEQ ID NO: 7

```

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```

151 <211> LENGTH: 21
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: PCR Primer
156 <400> SEQUENCE: 7
157     caacggattt ggtcgtattg g                                     21
159 <210> SEQ ID NO: 8
160 <211> LENGTH: 26
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: PCR Primer
165 <400> SEQUENCE: 8
166     ggcaacaata tccactttac cagagt                                     26
168 <210> SEQ ID NO: 9
169 <211> LENGTH: 21
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: PCR Probe
174 <400> SEQUENCE: 9
175     cgcctgggtca ccagggctgc t                                     21
177 <210> SEQ ID NO: 10
178 <211> LENGTH: 2006
179 <212> TYPE: DNA
180 <213> ORGANISM: Mus musculus
181 <220> FEATURE:
182 <221> NAME/KEY: CDS
183 <222> LOCATION: (474)...(1496)
184 <400> SEQUENCE: 10
185     agctcagtga ggctgatgtg tactgcacat ttaaaaaaaaa aatcacagga attttcatac      60
186     aatgaataaa accacaacaa tacatgtaga attggcaggt ggaaaagagc cagcaagggc      120
187     tcaaaactaat cactcacttt ccctcttcag catagttcaa ccaacagtag cacactttca      180
188     cctacaaatc ttaaagtagc tccatcaaat ctgcagtttt cacattattg aaaatgtctg      240
189     tcacataggt acaaatttag aatcatcaca ttatattaca tggctattct aggtcatcta      300
190     tagatcagat cttagactac agtgattgaa gttcttcgta cagccatcaa aaagggacac      360
191     atgatcatta cttactgtta gtcacatct aaaggcatga aaaggtttcc tttttttcaa      420
192     ctgaccctaaa cactttaccc caatagtgcc aggttcctc tctgctgctt tga atg      476
193                                     Met
194                                     1
195     ttc aca gcc caa gtg ttc tca gag tcc ttt aca aaa act gag ttg ctg      524
196     Phe Thr Ala Gln Val Phe Ser Glu Ser Phe Thr Lys Thr Glu Leu Leu
197           5                10                15
198     ccc tcg acc ctt gcg gag gac gga cgc tgc cgt ggg ctc ctg gcc gcc      572
199     Pro Ser Thr Leu Ala Glu Asp Gly Arg Cys Arg Gly Leu Leu Ala Ala
200           20                25                30
201     gcc gtg gga acg atg acc gat gat cag gac tgt gct gcg gag ctg gaa      620
202     Ala Val Gly Thr Met Thr Asp Asp Gln Asp Cys Ala Ala Glu Leu Glu

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203	35	40	45	
204	aag gtg gat tct tcc agc gaa gac gga gtt gac gcc aag cca gac cgc	668		
205	Lys Val Asp Ser Ser Ser Glu Asp Gly Val Asp Ala Lys Pro Asp Arg			
206	50	55	60	65
207	tcc tct atc atc tcc tct att ctc ttg aag aag aag aga aat gcc tct	716		
208	Ser Ser Ile Ile Ser Ser Ile Leu Leu Lys Lys Lys Arg Asn Ala Ser			
209	70	75	80	
210	gcg ggc ccc gtc agg acc ggc cgg gac cga gtg ccc act tat ctg tac	764		
211	Ala Gly Pro Val Arg Thr Gly Arg Asp Arg Val Pro Thr Tyr Leu Tyr			
212	85	90	95	
213	cgc atg gat ttc cag aag atg ggt aaa tgc atc atc ata aac aac aag	812		
214	Arg Met Asp Phe Gln Lys Met Gly Lys Cys Ile Ile Ile Asn Asn Lys			
215	100	105	110	
216	aac ttc gac aaa gcg aca ggt atg gac gtc cgg aat ggg acg gac aaa	860		
217	Asn Phe Asp Lys Ala Thr Gly Met Asp Val Arg Asn Gly Thr Asp Lys			
218	115	120	125	
219	gat gca ggg gcc ctc ttc aag tgc ttc caa aac ctg ggt ttt gaa gta	908		
220	Asp Ala Gly Ala Leu Phe Lys Cys Phe Gln Asn Leu Gly Phe Glu Val			
221	130	135	140	145
222	acc gtc cac aat gac tgc tct tgt gca aag atg caa gat ctg ctt aga	956		
223	Thr Val His Asn Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Arg			
224	150	155	160	
225	aaa gcc tct gag gag gac cac agc aac tcg gcc tgc ttc gcc tgc gtc	1004		
226	Lys Ala Ser Glu Asp His Ser Asn Ser Ala Cys Phe Ala Cys Val			
227	165	170	175	
228	ctg ctg agc cac ggg gaa gag gac ctg att tac ggg aaa gat ggc gtg	1052		
229	Leu Leu Ser His Gly Glu Glu Asp Leu Ile Tyr Gly Lys Asp Gly Val			
230	180	185	190	
231	aca ccc ata aag gat ctg aca gct cat ttt agg gga gac cga tgc aaa	1100		
232	Thr Pro Ile Lys Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys			
233	195	200	205	
234	acc ctg tta gag aaa ccc aaa ctc ttc ttc att cag gca tgc cga ggg	1148		
235	Thr Leu Leu Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly			
236	210	215	220	225
237	acg gag ctc gac gat gga atc cag gct gac tcg ggg ccc atc aac gac	1196		
238	Thr Glu Leu Asp Asp Gly Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp			
239	230	235	240	
240	att gac gct aat ccc cgc aac aag atc ccg gtg gaa gcc gac ttc ctc	1244		
241	Ile Asp Ala Asn Pro Arg Asn Lys Ile Pro Val Glu Ala Asp Phe Leu			
242	245	250	255	
243	ttt gct tac tcc acg gtt cca ggt tat tac tca tgg agg aac cca ggg	1292		
244	Phe Ala Tyr Ser Thr Val Pro Gly Tyr Tyr Ser Trp Arg Asn Pro Gly			
245	260	265	270	
246	aaa ggc tcc tgg ttt gtg cag gcc ctc tgc tcc atc ctg aat gag cat	1340		
247	Lys Gly Ser Trp Phe Val Gln Ala Leu Cys Ser Ile Leu Asn Glu His			
248	275	280	285	
249	ggc aag gac ctc gag atc atg cag atc ctg acc agg gtg aac gac agg	1388		
250	Gly Lys Asp Leu Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg			
251	290	295	300	305

**VERIFICATION SUMMARY**

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